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LIST OF CLAIMS, SHOWING THE STATUS OF EACH CLAIM

Underlining denotes added text while strikethrough denotes deleted text.

IN THE CLAIMS:

1. (Currently Amended) A cutinase variant comprising substitution of ~~one or more~~
~~amine acids at~~ residue positions corresponding to sites 192 and/or 194 and 192, of
Pseudomonas mendocina cutinase SEQ ID NO: 2, and wherein said variant has polyesterase
activity.

2. (Previously Presented) The cutinase of claim 1 isolated from
Pseudomonas mendocina.

3. (Cancelled)

4. (Cancelled)

5. (Cancelled)

6. (Cancelled)

7. (Cancelled)

8. (Cancelled)

9. (Previously Presented) The cutinase of claim 1, wherein said variant has
enhanced thermostability in comparison with wild-type *P. mendocina* cutinase.

10. (Cancelled)

11. (Cancelled)

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12. (Cancelled)

13. (Cancelled)

14. (Cancelled)

15. (Cancelled)

16. (Cancelled)

17. (Cancelled)

18. (Cancelled)

19. (Currently Amended) The cutinase of claim 1, wherein said variant comprises the following substitutions: Met at position 192, Val at position 194, and Ser at position 219 ~~He-192 with Met, Phe 194 with Val, and Ser 219 with Gly~~, wherein said variant has enhanced polyesterase activity, in comparison with wild-type *P. mendocina* cutinase.

20. (Cancelled)

21. (Cancelled)

22. (Cancelled)

23. (Cancelled)

24. (Cancelled)

25. (Cancelled)

26. (Cancelled)

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27. (Currently Amended) The cutinase of claim 1, wherein said variant comprises ~~includes the a~~ substitution of ~~Phe~~ the residue at position 194 with one of Ile, Leu, Asn, or Pro, wherein said variant has enhanced thermostability, in comparison with wild-type *P. mendocina* cutinase.

28. (Currently Amended) A cutinase variant comprising substitution ~~of one or more~~ amino acids at residue positions corresponding to sites 192 and/or 194 ~~and 192~~, of *Pseudomonas mendocina* cutinase SEQ ID NO: 2, and wherein said variant is more thermostable than wild-type cutinase, and has hydrolytic activity on polyester.

29. (Previously Presented) The cutinase variant of claim 28 isolated from *Pseudomonas* species.

30. (Previously Presented) The cutinase of claim 28, wherein said variant further comprises a substitution of the amino acid residue at position 219 of *Pseudomonas mendocina* cutinase SEQ ID NO: 2.

31. (Previously Presented) The cutinase of claim 1, wherein said variant further comprises a substitution of the amino acid residue at position 219 of *Pseudomonas mendocina* cutinase SEQ ID NO: 2.

32. (Previously Presented) The cutinase of claim 31, wherein said variant has enhanced thermostability in comparison with wild-type *P. mendocina* cutinase.

33. (Currently Amended) The cutinase of claim 30, wherein ~~Phe~~ the residue at ~~positon~~ 194 is substituted with one of Ala, His, Lys, Leu, Asn, Pro or Gly, and said ~~Ser~~ residue at position 219 is substituted with Gly.

34. (Currently Amended) The cutinase of claim 1, wherein said variant comprises ~~includes the a~~ substitution of ~~Phe~~ of the residue at position 194 with one of Ala or His, and a substitution of ~~Ser~~ at 219 with Gly, wherein said variant has enhanced polyesterase activity in comparison with wild-type *P. mendocina* cutinase.

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35. (Currently Amended) The cutinase of claim 1, wherein said variant ~~includes the~~ comprises a substitution of Phe at position 194 with Ile, wherein said variant has enhanced polyesterase activity in comparison with wild-type *P. mendocina* cutinase.

36. (Currently Amended) The cutinase of claim 1, wherein said variant ~~includes the~~ comprises a substitution of Phe at position 194 with one of Lys or Leu and substitution of ~~Ser at position 219~~ with Gly wherein said variant has enhanced polyesterase activity in comparison with wild-type *P. mendocina* cutinase.

37. (Currently Amended) The cutinase of claim 1, wherein said variant ~~includes~~ comprises the substitution of Asn at position 194 with Asn, wherein said variant has enhanced polyesterase activity in comparison with wild-type *P. mendocina* cutinase.

38. (Currently Amended) The cutinase of claim 1, wherein said variant ~~includes~~ comprises the substitution of Phe the residue at position 194 with one of Asn, Pro, or Ser, and substitution of the residue at position Ser 219 with Gly, wherein said variant has enhanced polyesterase activity in comparison with wild-type *P. mendocina* cutinase.